

SEQUENCE LISTING

<110> MEIJI SEIKA KAISHA, LTD.

<120> Endoglucanase and cellulase composition containing the same

<130> 121659PX

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<150> JP302387/1998

<151> 1998-10-23

<160> 113

<170> PatentIn Ver. 2.0

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<211> 338

<212> PRT

<213> Rhizopus oryzae CP96001

<220>

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<222> (-23)..(-1)

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Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Ser Gly
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Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys Lys Thr Thr Thr
45 50 55

Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr
60 65 70

Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala Ser Thr Pro Ser
75 80 85

Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala Val Ser Gly Gly
90 95 100 105

Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala
110 115 120

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Ser Cys Ser Trp Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser
125 130 135

Cys Asn Lys Asp Gly Val Thr Ala Leu Ser Asp Ser Asn Ala Gln Ser
140 145 150

Gly Cys Asn Gly Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp
155 160 165

Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser
170 175 180 185

Gly Gly Gly Glu Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe
190 195 200

Thr Ser Thr Ser Val Ala Gly Lys Lys Met Val Val Gln Val Thr Asn
205 210 215

Thr Gly Gly Asp Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln
220 225 230

Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Ser Gln Trp
235 240 245

Gly Ala Pro Asn Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser
250 255 260 265

Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys
270 275 280

Trp Arg Phe Asn Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr
285 290 295

Lys Glu Val Thr Cys Pro Lys Glu Ile Thr Ala Lys Thr Gly Cys Ser
300 305 310

Arg Lys
315

<210> 2
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<212> DNA
<213> Rhizopus oryzae CP96001

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<221> mat_peptide
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ggt act gaa atg gcc tct gct gct gaa tgt agc aaa ttg tat ggt caa 96
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-5 1 5

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acc tgt aaa gta agc aac gat tac tac tct caa tgt ctt ccc tct gga	192
Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Ser Gly	
30 35 40	
agc agt ggc aat aaa tct tct gaa agt gct cac aag aag act acc act	240
Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys Lys Thr Thr Thr	
45 50 55	
gct gct cac aag aag act act acc gct gct cat aaa aag act acc act	288
Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr	
60 65 70	
gct cct gct aag aag act aca act gtt gcc aaa gct tcc acc cct tct	336
Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala Ser Thr Pro Ser	
75 80 85	
aac tct agc tct agc tcc agc ggc aaa tat tcc gct gtc tct ggt ggt	384
Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala Val Ser Gly Gly	
90 95 100 105	
gcc tct ggt aac ggt gtc act act cgt tat tgg gat tgc tgt aag gcc	432
Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala	
110 115 120	
tcc tgt agc tgg ccc ggt aag gcc aat gtc agt tct cct gtc aag tcc	480
Ser Cys Ser Trp Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser	
125 130 135	
tgt aac aaa gat ggt gtc act gcc ctt agt gac agc aat gcc caa agt	528
Cys Asn Lys Asp Gly Val Thr Ala Leu Ser Asp Ser Asn Ala Gln Ser	
140 145 150	
ggc tgt aac ggt ggt aac agt tac atg tgt aac gac aac caa cct tgg	576
Gly Cys Asn Gly Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp	
155 160 165	
gct gta aac gac aac ctt gcc tat ggt ttc gct gct gct gcc atc agt	624
Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser	
170 175 180 185	
ggc ggt ggt gaa tct cgc tgg tgc tgt tct tgt ttc gaa ctt act ttc	672
Gly Gly Gly Glu Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe	
190 195 200	
act tct acc tct gtt gct ggt aag aag atg gtt gtc caa gtc act aac	720
Thr Ser Thr Ser Val Ala Gly Lys Lys Met Val Val Gln Val Thr Asn	
205 210 215	
act ggt ggt gat ctt ggc tcc tct act ggt gct cac ttt gac ttg caa	768
Thr Gly Gly Asp Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln	
220 225 230	
atg ccc ggt ggt ggt gtt ggt att ttc aat ggt tgt tcc agc caa tgg	816
Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Ser Gln Trp	
235 240 245	

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250                      255                      260                      265

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Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys
                      270                      275                      280

tgg aga ttc aac tgg ttc aag aac gct gat aac cca agc atg act tac      960
Trp Arg Phe Asn Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr
                      285                      290                      295

aag gaa gtt acc tgt cct aag gaa atc acc gcc aag aca ggt tgt tca     1008
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aga aaa taa
Arg Lys
315
1017

<210> 3
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<212> PRT
<213> Rhizopus oryzae CP96001

<220>
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<222> (-23)..(-1)
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Cys Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser
10                      15                      20                      25

Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu
30                      35                      40

Ser Asn Gly Asn Lys Ser Ser Glu Cys Ser Lys Leu Tyr Gly Gln Cys
45                      50                      55

Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr
60                      65                      70

Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu Ser
75                      80                      85

Asn Gly Asn Lys Thr Ser Glu Ser Ala His Lys Thr Thr Thr Thr Thr
90                      95                      100                      105

Ala Pro Ala Lys Glu Ile Thr Thr Thr Ala Lys Ala Ser Asn Ser Ser
110                      115                      120

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Asn Ser Ser Gly Lys Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly Asn
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Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala Ser Cys Ser Trp
140 145 150

Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser Cys Asn Lys Asp
155 160 165

Gly Val Thr Ala Leu Ser Asp Ser Asn Val Gln Ser Gly Cys Asn Gly
170 175 180 185

Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp Ala Val Asn Asp
190 195 200

Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser Gly Gly Gly Glu
205 210 215

Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe Thr Ser Thr Ser
220 225 230

Val Ala Gly Lys Lys Met Val Ile Gln Val Thr Asn Thr Gly Gly Asp
235 240 245

Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln Met Pro Gly Gly
250 255 260 265

Gly Val Gly Ile Phe Asn Gly Cys Ser Lys Gln Trp Gly Ala Pro Asn
270 275 280

Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser Ala Ser Asp Cys
285 290 295

Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys Trp Arg Phe Asn
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tgt ggt ggt aag gac tgg aat ggc cct act tgt tgc gaa tct gga tcc	144
Cys Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser	
10 15 20 25	
acc tgt aaa gta agc aac gat tac tac tct caa tgt ctt gcc cct gaa	192
Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu	
30 35 40	
agc aac ggc aat aag tct tct gaa tgt agc aag ttg tat ggt caa tgt	240
Ser Asn Gly Asn Lys Ser Ser Glu Cys Ser Lys Leu Tyr Gly Gln Cys	
45 50 55	
ggt ggt aag gac tgg aat ggc cct act tgt tgc gaa tct gga tcc acc	288
Gly Gly Lys Asp Trp Asn Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr	
60 65 70	
tgt aaa gta agc aac gat tac tac tct caa tgt ctt gcc cct gaa agc	336
Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Ala Pro Glu Ser	
75 80 85	
aat ggc aat aaa act tct gaa agc gct cat aaa acg act act acc act	384
Asn Gly Asn Lys Thr Ser Glu Ser Ala His Lys Thr Thr Thr Thr Thr	
90 95 100 105	
gct ccc gct aag gaa att aca act act gcc aaa gct tca aac tct tct	432
Ala Pro Ala Lys Glu Ile Thr Thr Thr Ala Lys Ala Ser Asn Ser Ser	
110 115 120	
aac tct agc ggc aaa tac tcc att gtc tct ggt ggt gcc tct ggt aac	480
Asn Ser Ser Gly Lys Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly Asn	
125 130 135	
ggt gtc act act cgt tat tgg gat tgc tgt aag gcc tcc tgt agc tgg	528
Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Ala Ser Cys Ser Trp	
140 145 150	
ccc ggt aag gcc aat gtc agt tct cct gtc aag tcc tgt aac aaa gat	576
Pro Gly Lys Ala Asn Val Ser Ser Pro Val Lys Ser Cys Asn Lys Asp	
155 160 165	
ggt gtc act gcc ctt agt gac agc aat gtc caa agt ggc tgt aac ggt	624
Gly Val Thr Ala Leu Ser Asp Ser Asn Val Gln Ser Gly Cys Asn Gly	
170 175 180 185	
ggt aac agt tac atg tgt aac gac aac cag cct tgg gct gta aac gat	672
Gly Asn Ser Tyr Met Cys Asn Asp Asn Gln Pro Trp Ala Val Asn Asp	
190 195 200	
aat ctt gcc tat ggt ttc gct gct gct gcc atc agt ggt ggt ggt gaa	720
Asn Leu Ala Tyr Gly Phe Ala Ala Ala Ala Ile Ser Gly Gly Gly Glu	
205 210 215	
tct cgc tgg tgc tgt tct tgt ttc gaa ctt act ttc act tct acc tct	768
Ser Arg Trp Cys Cys Ser Cys Phe Glu Leu Thr Phe Thr Ser Thr Ser	
220 225 230	

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235 240 245

ctt ggc tcc tct act ggt gct cac ttt gac ttg caa atg ccc ggt ggt 864
Leu Gly Ser Ser Thr Gly Ala His Phe Asp Leu Gln Met Pro Gly Gly
250 255 260 265

ggt gtt ggt att ttc aat ggt tgc tcc aag caa tgg ggt gct ccc aat 912
Gly Val Gly Ile Phe Asn Gly Cys Ser Lys Gln Trp Gly Ala Pro Asn
270 275 280

gac ggt tgg ggc tgc aga tac ggt ggt att tct tct gca tct gac tgc 960
Asp Gly Trp Gly Ser Arg Tyr Gly Gly Ile Ser Ser Ala Ser Asp Cys
285 290 295

tct agt ctt cct tcc gca ctc caa gct ggt tgt aaa tgg aga ttc aac 1008
Ser Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys Trp Arg Phe Asn
300 305 310

tgg ttc aag aac gct gat aac cca agc atg act tac aag gaa gtt acc 1056
Trp Phe Lys Asn Ala Asp Asn Pro Ser Met Thr Tyr Lys Glu Val Thr
315 320 325

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<213> Rhizopus oryzae CP96001

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30 35 40

Asn Glu Asn Leu Thr Ser Thr Asn Lys Ser Ser His Lys Thr Thr Thr
45 50 55

Thr Glu Ser Ala Lys Lys Thr Thr Thr Thr Lys Gly Ser Lys Lys Thr
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09807933SeqList.txt

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Lys Thr Thr Thr Thr Glu Ala Ser Lys Lys Thr Thr Thr Thr Thr Lys
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Lys Ala Ser Thr Ser Thr Ser Ser Ser Ser Ser Ala Ser Thr Asn
                               110                               115                               120

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly Asn Gly Glu Thr Thr Arg
                               125                               130                               135

Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ser Trp Pro Gly Lys Ala Asp
                               140                               145                               150

Val Thr Ser Pro Val Gly Ser Cys Asn Lys Asp Gly Lys Thr Leu Ala
                               155                               160                               165

Asp Asn Asn Thr Gln Asn Gly Cys Val Gly Gly Ser Ser Tyr Thr Cys
                               170                               175                               180                               185

Asn Asp Asn Gln Pro Trp Val Val Ser Asp Asp Leu Ala Tyr Gly Phe
                               190                               195                               200

Ala Ala Ala Ser Ile Ser Gly Gly Ser Glu Ala Thr Trp Cys Cys Ala
                               205                               210                               215

Cys Phe Glu Leu Thr Phe Thr Ser Thr Ala Val Lys Gly Lys Lys Met
                               220                               225                               230

Val Val Gln Val Thr Asn Thr Gly Ser Asp Leu Gly Ser Asn Thr Gly
                               235                               240                               245

Ala His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Ile Tyr Asn
                               250                               255                               260                               265

Gly Cys Ala Thr Gln Trp Gly Ala Pro Thr Asp Gly Trp Gly Ala Arg
                               270                               275                               280

Tyr Gly Gly Val Ser Ser Ala Ser Asp Cys Ser Asn Leu Pro Ser Ala
                               285                               290                               295

Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn Ala Asp
                               300                               305                               310

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Cys Gly Gly Lys Asn Trp Asp Gly Pro Thr Cys Cys Glu Ser Gly Ser	
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act tgc gtt gat tat cct gac aat cct ttc tac tcc caa tgt gtt ccc	192
Thr Cys Val Asp Tyr Pro Asp Asn Pro Phe Tyr Ser Gln Cys Val Pro	
30 35 40	
aat gaa aac ctc acc tcc act aac aaa tct tct cac aaa acc acc act	240
Asn Glu Asn Leu Thr Ser Thr Asn Lys Ser Ser His Lys Thr Thr Thr	
45 50 55	
act gag agt gcc aag aag act acc act act aaa ggt tcc aag aag acc	288
Thr Glu Ser Ala Lys Lys Thr Thr Thr Lys Gly Ser Lys Lys Thr	
60 65 70	
acc act act gaa gcc tct aag aag acc acc act act gaa gct tcc aag	336
Thr Thr Thr Glu Ala Ser Lys Lys Thr Thr Thr Thr Glu Ala Ser Lys	
75 80 85	
aag acc acc act act gaa gcc tct aag aag acc acc act act act aag	384
Lys Thr Thr Thr Thr Glu Ala Ser Lys Lys Thr Thr Thr Thr Thr Lys	
90 95 100 105	
aag gct tct acc tcc act tcc tct tcc tct tct tct gct tct aca aac	432
Lys Ala Ser Thr Ser Thr Ser Ser Ser Ser Ser Ser Ala Ser Thr Asn	
110 115 120	
tac tcc gct gtc tct ggt ggt gcc tcc ggt aat ggt gaa acc act cgc	480
Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly Asn Gly Glu Thr Thr Arg	
125 130 135	
tac tgg gat tgt tgt aag cct tct tgc agt tgg ccc ggt aag gct gat	528
Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ser Trp Pro Gly Lys Ala Asp	
140 145 150	
gtc acc tcc cct gtt ggc tcc tgt aac aag gat ggt aag act ctt gct	576
Val Thr Ser Pro Val Gly Ser Cys Asn Lys Asp Gly Lys Thr Leu Ala	
155 160 165	
gat aac aac act caa aac ggc tgt gtt ggt ggt agc agc tac acc tgt	624
Asp Asn Asn Thr Gln Asn Gly Cys Val Gly Gly Ser Ser Tyr Thr Cys	
170 175 180 185	
aat gac aat caa cct tgg gtt gtt agc gac gac ctt gcc tac ggt ttc	672
Asn Asp Asn Gln Pro Trp Val Val Ser Asp Asp Leu Ala Tyr Gly Phe	
190 195 200	

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Cys Phe Glu Leu Thr Phe Thr Ser Thr Ala Val Lys Gly Lys Lys Met
      220                      225                      230

gtt gtt caa gta acc aac act ggt tct gac ctt ggc tct aac act ggt 816
Val Val Gln Val Thr Asn Thr Gly Ser Asp Leu Gly Ser Asn Thr Gly
      235                      240                      245

gct cac ttt gac ttg caa atg ccc ggt ggt ggt gtt ggt atc tac aat 864
Ala His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Ile Tyr Asn
      250                      255                      260                      265

ggt tgt gcc act caa tgg ggt gct ccc acc gat ggt tgg ggt gca aga 912
Gly Cys Ala Thr Gln Trp Gly Ala Pro Thr Asp Gly Trp Gly Ala Arg
      270                      275                      280

tac ggc ggt gtt tct tct gcc tct gac tgt tct aac ctt cct tct gcc 960
Tyr Gly Gly Val Ser Ser Ala Ser Asp Cys Ser Asn Leu Pro Ser Ala
      285                      290                      295

ctt caa gct ggt tgt aag tgg aga ttc ggc tgg ttc aaa aac gct gat 1008
Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn Ala Asp
      300                      305                      310

aac cca acc atg acc tac aaa caa gtt acc tgt ccc aag gct atc act 1056
Asn Pro Thr Met Thr Tyr Lys Gln Val Thr Cys Pro Lys Ala Ile Thr
      315                      320                      325

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Ala Lys Ser Gly Cys Ser Arg Lys
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<213> Mucor circinelloides CP99001

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Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr
      15                      20                      25

Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro Gly

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09807933SeqList.txt

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35

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Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr Ser
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 60 65 70
 Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Lys Thr Ser Thr
 75 80 85 90
 Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ala Gly Tyr Lys Val
 95 100 105
 Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp Asp
 110 115 120
 Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr Gly
 125 130 135
 Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala Asn
 140 145 150
 Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn Asn
 155 160 165 170
 Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala Ala
 175 180 185
 Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr Glu
 190 195 200
 Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val Gln
 205 210 215
 Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu Gln
 220 225 230
 Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln Trp
 235 240 245 250
 Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser Ser
 255 260 265
 Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys
 270 275 280
 Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr Phe
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 Arg Lys
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<212> DNA

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<400> 8

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agc tct tct gct gaa gct gct tct tgc agc tct gtc tat ggt caa tgt 96
Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys
      -5                1                5                10

ggt ggc att gga tgg agt gga cct acc tgt tgt gaa agt ggc tct act 144
Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser Thr
                15                20                25

tgc gtt gct caa gaa ggc aac aaa tac tac tct caa tgt ctt ccc gga 192
Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro Gly
                30                35                40

tcc cac agt aac aat gct ggt aac gct agc agc acc aag aag aca tct 240
Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr Ser
                45                50                55

acc aag aca tct act acc acc gcc aag gct act gct act gtc acc acc 288
Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr Thr
                60                65                70

aag aca gta acc aag aca act acc aag aca act acc aag act agc act 336
Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser Thr
                75                80                85                90

act gcc gct gct tct act tcc acc tct tct tct gct ggt tac aag gtc 384
Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys Val
                95                100                105

atc tct ggc ggt aaa tct ggc agt ggt tcc aca act cgt tat tgg gat 432
Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp Asp
                110                115                120

tgt tgt aaa gct tct tgc agc tgg cct gga aaa gct tct gtc act ggt 480
Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr Gly
                125                130                135

cct gtt gac acc tgt gcc tcc aat ggt atc tct tta tta gat gcc aat 528
Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala Asn
                140                145                150

gct caa agt ggt tgt aac ggt ggt aat ggt ttc atg tgt aac aac aac 576
Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn Asn
                155                160                165                170

caa cct tgg gct gtc aat gat gag ctc gct tac ggt ttc gct gct gcc 624
Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala Ala

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09807933SeqList.txt

175	180	185	
tct att gct ggc tcc aac gaa gct gga tgg tgt tgt ggc tgt tat gaa Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr Glu	190	200	672
ttg acc ttc act tct ggc gct gct tct gga aag aag atg gtt gtt caa Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val Gln	205	215	720
gtt acc aac acc ggt ggc gat tta ggc tct aac cac ttt gat ttg caa Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu Gln	220	230	768
atg ccc ggt ggt ggc gtt ggt atc ttc aat ggc tgt gct gct caa tgg Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln Trp	235	245	816
ggc gct ccc aat gat ggc tgg gga gct aga tat ggt ggt gtc agc tct Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser Ser	255	265	864
gtc tct gac tgt gcc tct ctt ccc tct gct ctt caa gct ggt tgt aaa Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys Lys	270	280	912
tgg aga ttc aac tgg ttc aag aac tct gat aac cct acc atg acc ttc Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr Phe	285	295	960
aag gaa gtt acc tgt cct gct gaa tta act act cgc tca ggt tgc gaa Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys Glu	300	310	1008
aga aag taa Arg Lys			1017
315			
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Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys	-5	1	5
Gly Gly Ile Gly Trp Thr Gly Pro Thr Cys Cys Asp Ala Gly Ser Thr	15	20	25

09807933SeqList.txt

Cys Lys Ala Gln Lys Asp Asn Lys Tyr Tyr Ser Gln Cys Ile Pro Lys
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 Pro Lys Gly Ser Ser Ser Ser Ser Ser Cys Ser Ser Val Tyr Ser Gln
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 Cys Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser
 60 65 70
 Thr Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro
 75 80 85 90
 Gly Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr
 95 100 105
 Ser Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr
 110 115 120
 Thr Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser
 125 130 135
 Thr Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys
 140 145 150
 Val Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp
 155 160 165 170
 Asp Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr
 175 180 185
 Gly Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala
 190 195 200
 Asn Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn
 205 210 215
 Asn Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala
 220 225 230
 Ala Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr
 235 240 245 250
 Glu Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val
 255 260 265
 Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu
 270 275 280
 Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln
 285 290 295
 Trp Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser
 300 305 310
 Ser Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys
 315 320 325 330
 Lys Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr
 335 340 345

09807933SeqList.txt

Phe Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys
 350 355 360

Glu Arg Lys
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<222> (67)..(1164)

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agc tct tct gct gaa gct gct tct tgc agc tct gtc tat ggt caa tgt	96
Ser Ser Ser Ala Glu Ala Ala Ser Cys Ser Ser Val Tyr Gly Gln Cys	
-5 1 5 10	
ggc ggc att ggc tgg act ggt cct aca tgt tgt gat gct gga tcg acc	144
Gly Gly Ile Gly Trp Thr Gly Pro Thr Cys Cys Asp Ala Gly Ser Thr	
15 20 25	
tgt aaa gct caa aag gat aac aaa tat tat tct caa tgt att ccc aaa	192
Cys Lys Ala Gln Lys Asp Asn Lys Tyr Tyr Ser Gln Cys Ile Pro Lys	
30 35 40	
ccc aag ggt tcc tcc tca tca tca tca tgt agt tcc gtc tat agt caa	240
Pro Lys Gly Ser Ser Ser Ser Ser Ser Cys Ser Ser Val Tyr Ser Gln	
45 50 55	
tgc ggt ggc att gga tgg agt gga cct acc tgt tgt gaa agt ggc tct	288
Cys Gly Gly Ile Gly Trp Ser Gly Pro Thr Cys Cys Glu Ser Gly Ser	
60 65 70	
act tgc gtt gct caa gaa ggc aac aaa tac tac tct caa tgt ctt ccc	336
Thr Cys Val Ala Gln Glu Gly Asn Lys Tyr Tyr Ser Gln Cys Leu Pro	
75 80 85 90	
gga tcc cac agt aac aat gct ggt aac gct agc agc acc aag aag aca	384
Gly Ser His Ser Asn Asn Ala Gly Asn Ala Ser Ser Thr Lys Lys Thr	
95 100 105	
tct acc aag aca tct act acc acc gcc aag gct act gct act gtc acc	432
Ser Thr Lys Thr Ser Thr Thr Thr Ala Lys Ala Thr Ala Thr Val Thr	
110 115 120	
acc aag aca gta acc aag aca act acc aag aca act acc aag act agc	480
Thr Lys Thr Val Thr Lys Thr Thr Thr Lys Thr Thr Thr Lys Thr Ser	
125 130 135	

09807933SeqList.txt

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Thr Thr Ala Ala Ala Ser Thr Ser Thr Ser Ser Ser Ala Gly Tyr Lys	
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Val Ile Ser Gly Gly Lys Ser Gly Ser Gly Ser Thr Thr Arg Tyr Trp	
155 160 165 170	
gat tgt tgt aaa gct tct tgc agc tgg cct gga aaa gct tct gtc act	624
Asp Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Ser Val Thr	
175 180 185	
ggg cct gtt gac acc tgt gcc tcc aat ggt atc tct tta tta gat gcc	672
Gly Pro Val Asp Thr Cys Ala Ser Asn Gly Ile Ser Leu Leu Asp Ala	
190 195 200	
aat gct caa agt ggt tgt aac ggt ggt aat ggt ttc atg tgt aac aac	720
Asn Ala Gln Ser Gly Cys Asn Gly Gly Asn Gly Phe Met Cys Asn Asn	
205 210 215	
aac caa cct tgg gct gtc aat gat gag ctc gct tac ggt ttc gct gct	768
Asn Gln Pro Trp Ala Val Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala	
220 225 230	
gcc tct att gct ggc tcc aac gaa gct gga tgg tgt tgt ggc tgt tat	816
Ala Ser Ile Ala Gly Ser Asn Glu Ala Gly Trp Cys Cys Gly Cys Tyr	
235 240 245 250	
gaa ttg acc ttc act tct ggc gct gct tct gga aag aag atg gtt gtt	864
Glu Leu Thr Phe Thr Ser Gly Ala Ala Ser Gly Lys Lys Met Val Val	
255 260 265	
caa gtt acc aac acc ggt ggc gat tta ggc tct aac cac ttt gat ttg	912
Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Asn His Phe Asp Leu	
270 275 280	
caa atg ccc ggt ggt ggc gtt ggt atc ttc aat ggc tgt gct gct caa	960
Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ala Ala Gln	
285 290 295	
tgg ggc gct ccc aat gat ggc tgg gga gct aga tat ggt ggt gtc agc	1008
Trp Gly Ala Pro Asn Asp Gly Trp Gly Ala Arg Tyr Gly Gly Val Ser	
300 305 310	
tct gtc tct gac tgt gcc tct ctt ccc tct gct ctt caa gct ggt tgt	1056
Ser Val Ser Asp Cys Ala Ser Leu Pro Ser Ala Leu Gln Ala Gly Cys	
315 320 325 330	
aaa tgg aga ttc aac tgg ttc aag aac tct gat aac cct acc atg acc	1104
Lys Trp Arg Phe Asn Trp Phe Lys Asn Ser Asp Asn Pro Thr Met Thr	
335 340 345	
ttc aag gaa gtt acc tgt cct gct gaa tta act act cgc tca ggt tgc	1152
Phe Lys Glu Val Thr Cys Pro Ala Glu Leu Thr Thr Arg Ser Gly Cys	
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gaa aga aag taa	1164
Glu Arg Lys	
365	

09807933SeqList.txt

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<211> 346

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<213> Phycomyces nitens CP99002

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<221> sig_peptide

<222> (-19)..(-1)

<221> mat_peptide

<222> (1)..(327)

<400> 11

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          1                      5                      10

Met Trp Thr Gly Pro Thr Cys Cys Thr Ser Gly Phe Thr Cys Val Gly
          15                      20                      25

Ala Glu Asn Asn Glu Trp Tyr Ser Gln Cys Ile Pro Asn Asp Gln Val
          30                      35                      40                      45

Gln Gly Asn Pro Lys Thr Thr Thr Thr Thr Thr Thr Lys Ala Ala Thr
          50                      55                      60

Thr Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr
          65                      70                      75

Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr Thr
          80                      85                      90

Lys Thr Thr Thr Lys Thr Thr Thr Thr Lys Ala Ala Thr Thr Thr Ser
          95                      100                     105

Ser Ser Asn Thr Gly Tyr Ser Pro Ile Ser Gly Gly Phe Ser Gly Asn
110                      115                      120                     125

Gly Arg Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp
          130                      135                     140

Asp Gly Lys Ala Ser Val Thr Lys Pro Val Leu Thr Cys Ala Lys Asp
          145                      150                     155

Gly Val Ser Arg Leu Gly Ser Asp Val Gln Ser Gly Cys Val Gly Gly
          160                      165                     170

Gln Ala Tyr Met Cys Asn Asp Asn Gln Pro Trp Val Val Asn Asp Asp
          175                      180                     185

Leu Ala Tyr Gly Phe Ala Ala Ala Ser Leu Gly Ser Ala Gly Ala Ser
190                      195                     200                     205

Ala Phe Cys Cys Gly Cys Tyr Glu Leu Thr Phe Thr Asn Thr Ala Val
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Ala Gly Lys Lys Phe Val Val Gln Val Thr Asn Thr Gly Asp Asp Leu

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09807933SeqList.txt

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225                               230                               235
Ser Thr Asn His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Tyr
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Phe Asn Gly Cys Gln Ser Gln Trp Asn Thr Asn Thr Asp Gly Trp Gly
  255                               260                               265

Ala Arg Tyr Gly Gly Ile Ser Ser Ile Ser Glu Cys Asp Lys Leu Pro
  270                               275                               280                               285

Thr Gln Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn
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Ala Asp Asn Pro Glu Val Thr Phe Lys Ala Val Thr Cys Pro Ala Glu
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      -15                               -10                               -5

act tac gct gct gaa tgc agc caa ggc tat ggc cag tgt ggt ggc aag   96
Thr Tyr Ala Ala Glu Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys
      1                               5                               10

atg tgg act ggt ccc acc tgc tgc acc tcc ggc ttc acc tgt gta ggt   144
Met Trp Thr Gly Pro Thr Cys Cys Thr Ser Gly Phe Thr Cys Val Gly
      15                               20                               25

gcc gaa aac aac gag tgg tac tct cag tgt atc ccc aac gat caa gtc   192
Ala Glu Asn Asn Glu Trp Tyr Ser Gln Cys Ile Pro Asn Asp Gln Val
      30                               35                               40                               45

cag ggt aac ccc aag acc acc acc acc acc acc acc aag gct gcc act   240
Gln Gly Asn Pro Lys Thr Thr Thr Thr Thr Thr Thr Lys Ala Ala Thr
      50                               55                               60

acc acc aag gct cct gtc acc acc acc aag gcc acc acc acc acc acc   288
Thr Thr Lys Ala Pro Val Thr Thr Thr Thr Lys Ala Thr Thr Thr Thr
      65                               70                               75

acc aag gcc cct gtc acc acc acc aag gcc act act act acc acc acc   336
Thr Lys Ala Pro Val Thr Thr Thr Lys Ala Thr Thr Thr Thr Thr Thr
      80                               85                               90

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09807933SeqList.txt

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Ser Ser Asn Thr Gly Tyr Ser Pro Ile Ser Gly Gly Phe Ser Gly Asn	
110 115 120 125	
ggt cgc act acc cgc tac tgg gat tgc tgc aag ccc tct tgc gcc tgg	480
Gly Arg Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp	
130 135 140	
gac gga aag gct tct gta act aag cct gta ctc acc tgt gcc aag gat	528
Asp Gly Lys Ala Ser Val Thr Lys Pro Val Leu Thr Cys Ala Lys Asp	
145 150 155	
ggt gtc agc cgt ctc ggt tcc gat gtc cag agc ggt tgc gtc ggc ggc	576
Gly Val Ser Arg Leu Gly Ser Asp Val Gln Ser Gly Cys Val Gly Gly	
160 165 170	
cag gcc tac atg tgc aat gac aac cag ccc tgg gtt gtc aat gac gac	624
Gln Ala Tyr Met Cys Asn Asp Asn Gln Pro Trp Val Val Asn Asp Asp	
175 180 185	
ctt gcc tac ggt ttc gct gct gcc agt ctc ggt agc gcc ggt gcc tct	672
Leu Ala Tyr Gly Phe Ala Ala Ala Ser Leu Gly Ser Ala Gly Ala Ser	
190 195 200 205	
gca ttc tgc tgc ggc tgt tac gag ctt acc ttc acc aac act gct gtc	720
Ala Phe Cys Cys Gly Cys Tyr Glu Leu Thr Phe Thr Asn Thr Ala Val	
210 215 220	
gct ggc aag aag ttt gtc gtc cag gtc acc aac acc ggt gat gat ctc	768
Ala Gly Lys Lys Phe Val Val Gln Val Thr Asn Thr Gly Asp Asp Leu	
225 230 235	
agc acc aac cac ttt gat ttg cag atg ccc ggc ggt ggt gtc ggc tac	816
Ser Thr Asn His Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Tyr	
240 245 250	
ttc aac ggc tgc cag tcc cag tgg aac acc aac acc gat ggc tgg ggt	864
Phe Asn Gly Cys Gln Ser Gln Trp Asn Thr Asn Thr Asp Gly Trp Gly	
255 260 265	
gct cgc tat ggc ggt att agc tct att tca gag tgc gac aag ctt cct	912
Ala Arg Tyr Gly Gly Ile Ser Ser Ile Ser Glu Cys Asp Lys Leu Pro	
270 275 280 285	
acc cag ttg cag gct ggt tgc aag tgg aga ttc gga tgg ttc aag aac	960
Thr Gln Leu Gln Ala Gly Cys Lys Trp Arg Phe Gly Trp Phe Lys Asn	
290 295 300	
gct gac aac cca gag gtc acc ttc aag gct gtt act tgc cct gcc gag	1008
Ala Asp Asn Pro Glu Val Thr Phe Lys Ala Val Thr Cys Pro Ala Glu	
305 310 315	
atc att gcc aag act ggt tgc gag cgc aag taa	1041
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320

325

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<211> 1043

<212> DNA

<213> Artificial Sequence

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<221> mat_peptide

<222> (84)..(1043)

<223> Codon-optimized sequence corresponding to RCE I protein
(SEQ. ID NO:2)

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 Ala Leu Ala Leu Gly Thr Glu Met Ala Ser Ala Ala Glu Cys Ser Lys
 -10 -5 1 5

ctc tac gga cag tgc ggc gga aag aac tgg aac ggc ccc acc tgc tgc 147
 Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn Gly Pro Thr Cys Cys
 10 15 20

gag agc ggc tcg acc tgc aag gtc tcg aat gac tac tac agc cag tgc 195
 Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr Ser Gln Cys
 25 30 35

ctg ccg agc ggc tcc tcg gga aac aag tcg agc gag tcg gcc cac aag 243
 Leu Pro Ser Gly Ser Ser Gly Asn Lys Ser Ser Glu Ser Ala His Lys
 40 45 50

aag acc acg acc gct gcc cac aag aag acc acg acc gcc gct cac aag 291
 Lys Thr Thr Thr Ala Ala His Lys Lys Thr Thr Thr Ala Ala His Lys
 55 60 65

aag act acg acc gct ccc gcc aag aag acc acg acc gtc gcc aag gct 339
 Lys Thr Thr Thr Ala Pro Ala Lys Lys Thr Thr Thr Val Ala Lys Ala
 70 75 80 85

tcg act ccg tcc aac tcg agc agc tcg tct tcg gga aag tac agc gct 387
 Ser Thr Pro Ser Asn Ser Ser Ser Ser Ser Ser Gly Lys Tyr Ser Ala
 90 95 100

gtc agc ggt ggc gct agc ggc aac ggc gtc act acc cgc tac tgg gac 435
 Val Ser Gly Gly Ala Ser Gly Asn Gly Val Thr Thr Arg Tyr Trp Asp
 105 110 115

tgc tgc aag gct tcg tgc tcg tgg ccc ggc aag gct aac gtc agc tcg 483
 Cys Cys Lys Ala Ser Cys Ser Trp Pro Gly Lys Ala Asn Val Ser Ser
 120 125 130

cct gtc aag tcc tgc aac aag gac ggc gtc acc gct ctt agc gac tcc 531
 Pro Val Lys Ser Cys Asn Lys Asp Gly Val Thr Ala Leu Ser Asp Ser
 135 140 145

09807933SeqList.txt

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aac cag cca tgg gct gtc aac gac aac ctt gct tac ggt ttc gct gcc 627
Asn Gln Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala
170 175 180

gct gcc att agc ggc ggt ggc gag agc cgc tgg tgc tgc tcc tgc ttc 675
Ala Ala Ile Ser Gly Gly Gly Glu Ser Arg Trp Cys Cys Ser Cys Phe
185 190 195

gag ctc acc ttc acc tcc acc agc gtt gct ggc aag aag atg gtc gtc 723
Glu Leu Thr Phe Thr Ser Thr Ser Val Ala Gly Lys Lys Met Val Val
200 205 210

cag gtc acc aac act ggc ggt gac ctt ggc agc tcg acc ggt gcc cac 771
Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Ser Ser Thr Gly Ala His
215 220 225

ttc gat ctc cag atg ccc ggc ggc ggc gtc ggc atc ttc aac gga tgc 819
Phe Asp Leu Gln Met Pro Gly Gly Gly Val Gly Ile Phe Asn Gly Cys
230 235 240 245

tcg tcc cag tgg ggc gct ccc aac gac ggc tgg ggc tcg cgc tac ggc 867
Ser Ser Gln Trp Gly Ala Pro Asn Asp Gly Trp Gly Ser Arg Tyr Gly
250 255 260

ggc atc agc tcc gcc agc gac tgc tcg tcc ctc ccc agc gcc ctc cag 915
Gly Ile Ser Ser Ala Ser Asp Cys Ser Ser Leu Pro Ser Ala Leu Gln
265 270 275

gcc ggc tgc aag tgg cgc ttc aac tgg ttc aag aac gcc gac aac ccg 963
Ala Gly Cys Lys Trp Arg Phe Asn Trp Phe Lys Asn Ala Asp Asn Pro
280 285 290

tcc atg acc tac aag gag gtc acc tgc ccc aag gag atc acc gct aag 1011
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295 300 305

acc gga tgc tcg cgc aag taaacgcagg atcc 1043
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<212> PRT

<213> Rhizopus oryzae CP96001

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Tyr Tyr Ser Gln Cys Leu Pro Ser

35

40

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 <213> Phycomyces nitens CP99002

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 1 5 10 15

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<210> 17
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 <212> PRT
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<220>

09807933SeqList.txt

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<223> any amino acid or empty

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          20             25             30
Xaa Xaa Tyr Xaa Gln Cys Xaa
          35

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<212> PRT
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<223> any amino acid

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<220>
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Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asn
      20                      25                      30
Xaa Xaa Tyr Xaa Gln Cys Xaa
      35

<210> 19
<211> 38
<212> PRT
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<220>
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      sequence (CBD)

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09807933SeqList.txt

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<222> (26)..(28)
<223> any amino acid

<220>
<221> MISC_FEATURE
<222> (29)..(30)
<223> any amino acid or empty

<220>
<221> MISC_FEATURE
<222> (32)..(33)
<223> any amino acid

<220>
<221> MISC_FEATURE
<222> (38)
<223> any amino acid

<400> 19
Cys Ser Xaa Xaa Tyr Xaa Gln Cys Gly Gly Xaa Xaa Trp Xaa Gly Pro
 1             5             10             15

Thr Cys Cys Xaa Xaa Gly Xaa Thr Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa
 20             25             30

Xaa Tyr Ser Gln Cys Xaa

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<210> 20
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
sequence (CBD)

<220>
<221> MISC_FEATURE
<222> (3)
<223> Lys, Ser or Gln

<220>
<221> MISC_FEATURE
<222> (4)
<223> Leu, Ala, Val or Gly

<220>
<221> MISC_FEATURE
<222> (6)
<223> Gly, Tyr or Ser

<220>
<221> MISC_FEATURE
<222> (11)
<223> Lys or Ile

<220>
<221> MISC_FEATURE
<222> (12)
<223> Asn, Asp, Gly or Met

<220>
<221> MISC_FEATURE
<222> (14)
<223> Asn, Asp, Ser or Thr

<220>
<221> MISC_FEATURE
<222> (20)
<223> Glu, Asp or Thr

<220>
<221> MISC_FEATURE
<222> (21)
<223> Ser or Ala

<220>
<221> MISC_FEATURE
<222> (23)
<223> Ser or Phe

<220>

<221> MISC_FEATURE

<222> (26)

<223> Lys or Val

<220>

<221> MISC_FEATURE

<222> (27)

<223> Val, Asp, Ala or Gly

<220>

<221> MISC_FEATURE

<222> (28)

<223> Ser, Tyr, Gln or Ala

<220>

<221> MISC_FEATURE

<222> (29)

<223> Pro, Glu, Lys or absent

<220>

<221> MISC_FEATURE

<222> (30)

<223> Asp, Gly, Asn or absent

<221> MISC_FEATURE

<222> (32)

<223> Asp, Pro, Lys or Glu

<220>

<221> MISC_FEATURE

<222> (33)

<223> Tyr, Phe or Trp

<220>

<221> MISC_FEATURE

<222> (38)

<223> Leu, Val or Ile

<400> 20

Cys	Ser	Xaa	Xaa	Tyr	Xaa	Gln	Cys	Gly	Gly	Xaa	Xaa	Trp	Xaa	Gly	Pro
1				5					10					15	

Thr	Cys	Cys	Xaa	Xaa	Gly	Xaa	Thr	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa
			20					25					30		

Xaa	Tyr	Ser	Gln	Cys	Xaa
					35

<210> 21

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence (CBD)

<220>
<221> MISC_FEATURE
<222> (4)
<223> Leu or Ala

<220>
<221> MISC_FEATURE
<222> (6)
<223> Gly or Tyr

<220>
<221> MISC_FEATURE
<222> (12)
<223> Asn or Asp

<220>
<221> MISC_FEATURE
<222> (14)
<223> Asn or Asp

<220>
<221> MISC_FEATURE
<222> (26)
<223> Lys or Val

<220>
<221> MISC_FEATURE
<222> (27)
<223> Val or Asp

<220>
<221> MISC_FEATURE
<222> (28)
<223> Ser or Tyr

<220>
<221> MISC_FEATURE
<222> (29)
<223> Pro or absent

<220>
<221> MISC_FEATURE
<222> (30)
<223> Asp or absent

<220>
<221> MISC_FEATURE
<222> (32)
<223> Asp or Pro

<220>
<221> MISC_FEATURE
<222> (33)
<223> Tyr or Phe

<220>
<221> MISC_FEATURE
<222> (38)
<223> Leu or Val

09807933SeqList.txt

<400> 21

Cys Ser Lys Xaa Tyr Xaa Gln Cys Gly Gly Lys Xaa Trp Xaa Gly Pro
1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa
20 25 30

Xaa Tyr Ser Gln Cys Xaa
35

<210> 22

<211> 36

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 22

Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn Gly Pro
1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr
20 25 30

Ser Gln Cys Leu
35

<210> 23

<211> 36

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 23

Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asp Trp Asn Gly Pro
1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Lys Val Ser Asn Asp Tyr Tyr
20 25 30

Ser Gln Cys Leu
35

<210> 24

<211> 38

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 24

Cys Ser Lys Ala Tyr Tyr Gln Cys Gly Gly Lys Asn Trp Asp Gly Pro
1 5 10 15

Thr Cys Cys Glu Ser Gly Ser Thr Cys Val Asp Tyr Pro Asp Asn Pro
20 25 30

Phe Tyr Ser Gln Cys Val
35

09807933SeqList.txt

<210> 25
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 sequence (CBD)

<220>
 <221> MISC_FEATURE
 <222> (6)
 <223> Gly or Ser

<220>
 <221> MISC_FEATURE
 <222> (14)
 <223> Ser or Thr

<220>
 <221> MISC_FEATURE
 <222> (20)
 <223> Glu or Asp

<220>
 <221> MISC_FEATURE
 <222> (21)
 <223> Ser or Ala

<220>
 <221> MISC_FEATURE
 <222> (26)
 <223> Val or Lys

<220>
 <221> MISC_FEATURE
 <222> (29)
 <223> Glu or Lys

<220>
 <221> MISC_FEATURE
 <222> (30)
 <223> Gly or Asp

<220>
 <221> MISC_FEATURE
 <222> (38)
 <223> Leu or Ile

<400> 25
 Cys Ser Ser Val Tyr Xaa Gln Cys Gly Gly Ile Gly Trp Xaa Gly Pro
 1 5 10 15
 Thr Cys Cys Xaa Xaa Gly Ser Thr Cys Xaa Ala Gln Xaa Xaa Asn Lys
 20 25 30
 Tyr Tyr Ser Gln Cys Xaa
 35

09807933SeqList.txt

<210> 26
 <211> 38
 <212> PRT
 <213> Mucor circinelloides CP99001

<400> 26
 Cys Ser Ser Val Tyr Gly Gln Cys Gly Gly Ile Gly Trp Ser Gly Pro
 1 5 10 15
 Thr Cys Cys Glu Ser Gly Ser Thr Cys Val Ala Gln Glu Gly Asn Lys
 20 25 30
 Tyr Tyr Ser Gln Cys Leu
 35

<210> 27
 <211> 38
 <212> PRT
 <213> Mucor circinelloides CP99001

<400> 27
 Cys Ser Ser Val Tyr Gly Gln Cys Gly Gly Ile Gly Trp Thr Gly Pro
 1 5 10 15
 Thr Cys Cys Asp Ala Gly Ser Thr Cys Lys Ala Gln Lys Asp Asn Lys
 20 25 30
 Tyr Tyr Ser Gln Cys Ile
 35

<210> 28
 <211> 38
 <212> PRT
 <213> Phycomyces nitens CP99002

<400> 28
 Cys Ser Gln Gly Tyr Gly Gln Cys Gly Gly Lys Met Trp Thr Gly Pro
 1 5 10 15
 Thr Cys Cys Thr Ser Gly Phe Thr Cys Val Gly Ala Glu Asn Asn Glu
 20 25 30
 Trp Tyr Ser Gln Cys Ile
 35

<210> 29
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 sequence (linker)

<220>
 <221> MISC_FEATURE
 <222> (1)
 <223> Ser, Thr or Ala

<220>
 <221> MISC_FEATURE
 <222> (5)
 <223> Trp, Tyr or Phe

<220>
 <221> MISC_FEATURE
 <222> (7)..(12)
 <223> any amino acid

<400> 29
 Xaa Thr Arg Tyr Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10

<210> 30
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 sequence (linker)

<220>
 <221> MISC_FEATURE
 <222> (2)..(4)
 <223> any amino acid

<220>
 <221> MISC_FEATURE
 <222> (8)
 <223> any amino acid

<400> 30
 Tyr Xaa Xaa Xaa Ser Gly Gly Xaa Ser Gly
 1 5 10

<210> 31
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 sequence (linker)

<220>
 <221> MISC_FEATURE
 <222> (2)..(4)
 <223> any amino acid

<220>

<221> MISC_FEATURE
<222> (5)
<223> Ser or Thr

<220>
<221> MISC_FEATURE
<222> (8)
<223> any amino acid

<220>
<221> MISC_FEATURE
<222> (9)
<223> Ser or Thr

<400> 31
Tyr Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Gly
1 5 10

<210> 32
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
sequence (linker)

<220>
<221> MISC_FEATURE
<222> (2)
<223> Lys or Ser

<220>
<221> MISC_FEATURE
<222> (3)
<223> any amino acid

<220>
<221> MISC_FEATURE
<222> (4)
<223> Ile or Val

<220>
<221> MISC_FEATURE
<222> (5)
<223> Ser or Thr

<220>
<221> MISC_FEATURE
<222> (8)
<223> any amino acid

<220>
<221> MISC_FEATURE
<222> (9)
<223> Ser or Thr

<400> 32

09807933SeqList.txt

Tyr Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Gly
1 5 10

<210> 33
<211> 10
<212> PRT
<213> Rhizopus oryzae CP96001

<400> 33
Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly
1 5 10

<210> 34
<211> 10
<212> PRT
<213> Rhizopus oryzae CP96001

<400> 34
Tyr Ser Ile Val Ser Gly Gly Ala Ser Gly
1 5 10

<210> 35
<211> 10
<212> PRT
<213> Mucor circinelloides CP99001

<400> 35
Tyr Lys Val Ile Ser Gly Gly Lys Ser Gly
1 5 10

<210> 36
<211> 10
<212> PRT
<213> Phycomyces nitens CP99002

<400> 36
Tyr Ser Pro Ile Ser Gly Gly Phe Ser Gly
1 5 10

<210> 37
<211> 26
<212> PRT
<213> Rhizopus oryzae CP96001

<400> 37
Ala Lys Ala Ser Thr Pro Ser Asn Ser Ser Ser Ser Ser Gly Lys
1 5 10 15

Tyr Ser Ala Val Ser Gly Gly Ala Ser Gly
20 25

<210> 38
<211> 10

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 38

Asn	Ala	Asp	Asn	Pro	Ser	Met	Thr	Tyr	Lys
1				5					10

<210> 39

<211> 10

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 39

Tyr	Ser	Ala	Val	Ser	Gly	Gly	Ala	Ser	Gly
1				5					10

<210> 40

<211> 17

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 40

Ser	Ala	Ser	Asp	Cys	Ser	Ser	Leu	Pro	Ser	Ala	Leu	Gln	Ala	Gly	Cys
1				5					10					15	

Lys

<210> 41

<211> 18

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 41

Tyr	Gly	Gly	Ile	Ser	Ser	Ala	Ser	Asp	Cys	Ser	Ser	Leu	Pro	Ser	Ala
1				5					10					15	

Leu Gln

<210> 42

<211> 6

<212> PRT

<213> Rhizopus oryzae CP96001

<400> 42

Arg	Phe	Asn	Trp	Phe	Lys
1				5	

<210> 43

<211> 20

<212> DNA

<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (15)..(15)
<223> inosine

<220>
<221> misc_feature
<222> (18)..(18)
<223> a, g, c or t

<400> 43
aaraaytgga ayggnccnac                                     20

<210> 44
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (15)
<223> a, g, c, or t

<400> 44
ttraaccart traancg                                         17

<210> 45
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 45
ttraaccart traayct                                         17

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 46
caatgtcttc cctctggaag cag                                   23

<210> 47

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09807933SeqList.txt

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<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 47
tgcccttagt gacagcaatg ccc                23

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 48
cttccttccg cactccaagc tgg                23

<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 49
ccagcttgga gtgcggaagg aag                23

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 50
tcactaaggg cagtgacacc atc                23

<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 51
cagagggaag acattgagag tag                23

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09807933SeqList.txt

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<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 52
acaacattat ttcttcaaac atg
23

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 53
aaatgccgca tcaagtttta ttg
23

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 54
ttcacttcta cctctgttgc tgg
23

<210> 55
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 55
gtaataaact tcatagatct atgtaaaaag aatg
34

<210> 56
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 56
ggatgagtat aaaagatctt attttcttga ac
32

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09807933SeqList.txt

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<210> 57
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 57
cactttcaga agctttattg ccac
24

<210> 58
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 58
gagctagagc cagagttaga ag
22

<210> 59
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 59
gagaactgac atcggcctta cc
22

<210> 60
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 60
acaacattat ttcttcgaat atg
23

<210> 61
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 61
ttagcagca gaggccattt cag
23

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09807933SeqList.txt

<210> 62
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 62
 ttttctatcc tgatacagag atg 23

<210> 63
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 63
 gcgctcataa aacgactact acc 23

<210> 64
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 64
 tgcccttagt gacagcaatg tcc 23

<210> 65
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 65
 caagaaaata agatctttta tactcctact 30

<210> 66
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 66

aacggcaata aggcctctga atgtagc 27

<210> 67
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 67
 gaaagcaatg gccagaaaac ttctgaaag 29

<210> 68
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 68
 gcttcaaact ctctagactc tagcggc 27

<210> 69
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 69
 cggttaaggcc gacgtcagtt ctcc 24

<210> 70
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 70
 tacaggagcc aacaggggag gtg 23

<210> 71
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 71
ttcacagcag gtaggtccat tcc 23

<210> 72
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 72
cctacggttt cgccgctgct tcc 23

<210> 73
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 73
tagataccaa caccaccacc ggg 23

<210> 74
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 74
tgaagttcct taccattgcc tcc 23

<210> 75
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 75
tggtgaaacc actcgctact ggg 23

<210> 76
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

09807933SeqList.txt

<400> 76
ttctgcctct gactgttcta acc 23

<210> 77
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 77
aatagagtta ctctatacga tag 23

<210> 78
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 78
caccaccaga gacagcggag tag 23

<210> 79
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 79
tgcgttgatt atcctgacaa tcc 23

<210> 80
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 80
gcggatccat gaagttcctt accattgcc 29

<210> 81
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 81

gcggatcctt attttcttga acagccaga

29

<210> 82

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 82

gtggaggtga gatcttcatt gggaac

26

<210> 83

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 83

cagcggagta cttttagaa gcag

24

<210> 84

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 84

gggagatctt gggacaagat gaagtttatt actattg

37

<210> 85

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 85

ggtcaaacia gtctgtgcgg atcctgggac aagatggcca agttcttcct tac

53

<210> 86

<211> 132

<212> DNA

<213> Artificial Sequence

09807933SeqList.txt

<220>

<223> Description of Artificial Sequence:primer

<400> 86

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gggggatacct gggacaagat gaagttcatc actatcgctt cctccgccct ccttgccctc 60
gcccttggca ctgagatggc ctccgccgct gagtgtcca agctctacgg ccagtgcggc 120
ggaaagaact gg                                     132

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<210> 87

<211> 136

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 87

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ggccgactcg ctcgacttgt ttcccagagga gccgctcggc aggcactggc tgtagtagtc 60
attcgagacc ttgcaggtcg agccgctctc gcagcagggtg gggccggttc agttctttcc 120
gccgactgg ccgtag                                     136

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<210> 88

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 88

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gggctcgagt tggacggagt cgaagccttg gcgacggctg tggctcttctt ggccgggagcg 60
gtcgtagtct tcttgtgagc ggcggctcgtg gtcttcttctt gggcagcggc cgtggtcttc 120
ttgtgggccg actcgtcga cttgtttccc                                     150

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<210> 89

<211> 158

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 89

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ggaaacaagt cgagcgagtc ggcccacaag aagaccacga ccgctgcca caagaagacc 60
acgaccgccg ctcaacaaga gactacgacc gctcccgcca agaagaccac gaccgtcgcc 120
aaggcttcga ctccgtcca ctcgagcagc tcgtcttc                                     158

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<210> 90

<211> 160

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

09807933SeqList.txt

<400> 90
gtccttggtg caggacttga caggcgagct gacgtagcc ttgccgggccc acgagcacga 60
agccttgtag cagtcaccagt agcgggtagt gacgccgttg ccgctagcgc caccgctgac 120
agcgtgtac tttcccagag acgagctgct cgagttggac 160

<210> 91
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 91
agcccatggc tggttgtcgt tgcacatgta ggagttgccg ccggtgcagc cggactgggc 60
gttgagagtcg ctaagagcgg tgacgccgctc cttggtgcag gacttgacag gcgagctgac 120

<210> 92
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 92
ggtgagctcg aagcaggagc agcaccagcg gctctcgcca ccgccgctaa tggcagcggc 60
agcgaaaccg taagcaaggc tgctggtgac agcccatggc tggttgtcgt tgcacatg 118

<210> 93
<211> 154
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 93
gtgcccactt cgatctccag atgcccggcg gcggcgctcg catcttcaac ggatgctcgt 60
cccagtgggg cgtcccaac gacggctggg gctcgcgcta cggcggcatc agtccgcca 120
gcgactgctc gtccctcccc agcgcctcc aggc 154

<210> 94
<211> 154
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 94
gggggggatcc tgcgtttact tgcgcgagca tccggcttta gcggtgatct ccttggggca 60
ggtgacctcc ttgtaggtca tggacggggt gtcggcgctt ttgaaccagt tgaagcgcca 120
cttgagccg gcctggaggg cgctggggag ggac 154

09807933SeqList.txt

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<210> 95
<211> 117
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 95
ggggagctca ccttcacctc caccagcggt gctggcaaga agatggtcgt ccaggtcacc 60
aacactggcg gtgaccttgg cagctcgacc ggtgcccact tcgatctcca gatgccc 117


<210> 96
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 96
gggggggatcc tgcgtttact tgcgcgagca tc 32


<210> 97
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 97
tcagcgggtgg cgctagcggc aac 23


<210> 98
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 98
ctaattggcag cggcagcgaa acc 23


<210> 99
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 99

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ccggtgcccc attogatctc cag 23

<210> 100
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 100
tctttccgcc gcactgtccg tag 23

<210> 101
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 101
acgacaacca gccatgggct gtc 23

<210> 102
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 102
tctcgaatga ctactacagc cag 23

<210> 103
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence:primer

<400> 103
cccactggga cgagcatccg ttg 23

<210> 104
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 104
cgagctgctc gagttggacg gag

23

<210> 105
<211> 16
<212> PRT
<213> Rhizopus oryzae CP96001

<400> 105
Ala Glu Cys Ser Lys Leu Tyr Gly Gln Cys Gly Gly Lys Asn Trp Asn
1 5 10 15

<210> 106
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 106
gactgaccgg tggatcatcc

19

<210> 107
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 107
ctcgggtgtc atagatgtgg

20

<210> 108
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 108
cccacagaag ggatccatga tggtcgc

27

<210> 109
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 109

gcgaattcat gaagttcacc gttgctatt

29

<210> 110

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 110

gcgaattctt actttctttc gcaacctg

28

<210> 111

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 111

cttggtgctg ccagcggtac cag

23

<210> 112

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 112

gcggatccat gaagttctcc atcatcg

27

<210> 113

<211> 27

<212> DNA

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<220>

<223> Description of Artificial Sequence:primer

<400> 113

gcggatcctt acttgcgctc gcaacca

27